

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 22:19:33 ; Search time 5440 Seconds
(without alignments)
11154.292 Million cell updates/sec

Title: US-09-846-589A-9
Perfect score: 2085
Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

Seq Search Summary
for Seq 9
Oligo

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

USPN 6255090

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2085	100.0	2085	6	AR160636	AR160636 Sequence
	2	32	1.5	1957	6	AR160637	AR160637 Sequence
	3	32	1.5	142373	2	AC122149	AC122149 Oryza sat
	4	32	1.5	261604	2	AC119819	AC119819 Mus muscu
c	5	32	1.5	261604	2	AC119819	AC119819 Mus muscu
	6	25	1.2	242	9	AF023663	AF023663 Macaca ra
	7	25	1.2	5737	3	DMU78088	U78088 Drosophila
c	8	25	1.2	8718	6	AX346174	AX346174 Sequence
	9	25	1.2	22578	2	AC015113	AC015113 Drosophil
c	10	25	1.2	80692	2	AC100569	AC100569 Mus muscu
c	11	25	1.2	86209	8	AP004523	AP004523 Lotus jap
	12	25	1.2	87767	2	AC014497	AC014497 Drosophil
	13	25	1.2	90608	2	AC128541	AC128541 Rattus no
	14	25	1.2	146893	2	CNS08C9A	AL732535 Oryza sat
	15	25	1.2	150347	2	AC027038	AC027038 Oryza sat
c	16	25	1.2	150587	3	AC007549	AC007549 Drosophil
c	17	25	1.2	179421	2	AC110690	AC110690 Rattus no
c	18	25	1.2	181771	3	AC008340	AC008340 Drosophil
c	19	25	1.2	187437	3	AC023751	AC023751 Drosophil
c	20	25	1.2	188781	10	AL713870	AL713870 Mouse DNA
c	21	25	1.2	215986	9	AP002379	AP002379 Homo sapi
c	22	25	1.2	301769	3	AE003482	AE003482 Drosophil
c	23	24	1.2	341	6	AX397195	AX397195 Sequence
	24	24	1.2	5671	3	AY119457	AY119457 Drosophil
	25	24	1.2	9700	9	AB032251	AB032251 Homo sapi
c	26	24	1.2	14947	2	AC014403	AC014403 Drosophil
	27	24	1.2	33038	3	U97016	U97016 Caenorhabdi
c	28	24	1.2	59843	8	AP000816	AP000816 Oryza sat
	29	24	1.2	62091	2	DMBR28018	AL121814 Drosophil
	30	24	1.2	71154	2	AC130323	AC130323 Homo sapi
	31	24	1.2	80692	2	AC100569	AC100569 Mus muscu
c	32	24	1.2	111191	2	AC127525	AC127525 Homo sapi
	33	24	1.2	119526	2	AC007468	AC007468 Drosophil

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 20:47:02 ; Search time 436 Seconds
(without alignments)
10769.304 Million cell updates/sec

Title: US-09-846-589A-9
Perfect score: 2085
Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

from USPN 6255090

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2085	100.0	2085	22	AAD07973	Corn cysteinyl-tRN
	2	112	5.4	294	24	ABL72570	Corn tassel-derive
	3	32	1.5	1957	22	AAD07974	Rice cysteinyl-tRN
c	4	25	1.2	902	24	ABQ46430	Oligonucleotide fo
	5	25	1.2	902	24	ABQ46431	Oligonucleotide fo
c	6	25	1.2	8718	24	ABL33272	Human immune syste
c	7	25	1.2	28360	23	ABL06142	Drosophila melanog
c	8	24	1.2	341	24	ABK45859	cDNA encoding colo
c	9	24	1.2	903	24	ABQ14804	Oligonucleotide fo
	10	24	1.2	903	24	ABQ14805	Oligonucleotide fo
	11	24	1.2	9700	21	AAZ39033	Human transcriptio
	12	24	1.2	9865	21	AAZ39032	Human transcriptio
	13	24	1.2	10314	23	ABL29797	Drosophila melanog
	14	24	1.2	13560	23	ABL28568	Drosophila melanog
	15	24	1.2	17729	23	ABL29796	Drosophila melanog
c	16	23	1.1	578	24	ABQ36480	Oligonucleotide fo
	17	23	1.1	578	24	ABQ36481	Oligonucleotide fo
c	18	23	1.1	12425	22	AAH26495	Human low density
c	19	23	1.1	14568	24	ABL32230	Human immune syste
c	20	23	1.1	14686	23	ABL15140	Drosophila melanog
	21	23	1.1	23710	23	ABL08132	Drosophila melanog
c	22	23	1.1	29329	22	ABA18026	Human nervous syst
c	23	23	1.1	29329	22	ABA20511	Human nervous syst
c	24	23	1.1	29329	22	AAK70791	Human immune/haema
c	25	23	1.1	29329	22	AAK78512	Human immune/haema
	26	22	1.1	494	21	AAC51742	Zea mays DNA fragm
c	27	22	1.1	586	24	ABQ50526	Oligonucleotide fo
	28	22	1.1	586	24	ABQ50527	Oligonucleotide fo
c	29	22	1.1	796	24	ABQ28404	Oligonucleotide fo
	30	22	1.1	796	24	ABQ28405	Oligonucleotide fo
c	31	22	1.1	958	24	ABQ43126	Oligonucleotide fo
	32	22	1.1	958	24	ABQ43127	Oligonucleotide fo
c	33	22	1.1	1147	24	ABQ42108	Oligonucleotide fo
	34	22	1.1	1147	24	ABQ42109	Oligonucleotide fo
c	35	22	1.1	1341	24	ABQ15050	Oligonucleotide fo
	36	22	1.1	1341	24	ABQ15051	Oligonucleotide fo
	37	22	1.1	1600	21	AAC44491	Zea mays DNA fragm
c	38	22	1.1	1618	24	ABQ39530	Oligonucleotide fo
	39	22	1.1	1618	24	ABQ39531	Oligonucleotide fo
	40	22	1.1	2366	22	AAK51465	Human polynucleoti
c	41	22	1.1	2406	22	AAK52449	Human polynucleoti
c	42	22	1.1	2500	24	ABN95898	Gene #2396 used to
c	43	22	1.1	2500	24	ABK72303	Lymphona associate
c	44	22	1.1	5391	24	ABK39939	Human chemically p
c	45	22	1.1	5391	24	ABL32243	Human immune syste

ALIGNMENTS

RESULT 1

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 20:59:21 ; Search time 81 Seconds
(without alignments)
7894.087 Million cell updates/sec

Title: US-09-846-589A-9
Perfect score: 2085
Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	2085	100.0	2085	4	US-09-352-990-9	Sequence 9, Appli	
2	32	1.5	1957	4	US-09-352-990-11	Sequence 11, Appl	
3	21	1.0	333	1	US-08-844-010-3	Sequence 3, Appli	
4	21	1.0	333	3	US-09-012-873-3	Sequence 3, Appli	
5	21	1.0	451	4	US-09-357-251-3	Sequence 3, Appli	
c 6	21	1.0	640	2	US-08-835-099A-16	Sequence 16, Appl	
c 7	21	1.0	640	3	US-09-157-349-16	Sequence 16, Appl	
c 8	21	1.0	804	2	US-08-835-099A-10	Sequence 10, Appl	
c 9	21	1.0	804	3	US-09-157-349-10	Sequence 10, Appl	
10	21	1.0	1070	4	US-09-470-443-7	Sequence 7, Appli	
11	21	1.0	1344	1	US-08-844-010-1	Sequence 1, Appli	
12	21	1.0	1344	3	US-09-012-873-1	Sequence 1, Appli	

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 22:30:12 ; Search time 97 Seconds
(without alignments)
9459.953 Million cell updates/sec

Title: US-09-846-589A-9
Perfect score: 2085
Sequence: 1 ggaaaccgtgttttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Word size : 0

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	249	11.9	249	10	US-09-923-876-1857	Sequence 1857, Ap
2	112	5.4	294	10	US-09-294-093B-1944	Sequence 1944, Ap
c 3	24	1.2	341	10	US-09-920-300A-1410	Sequence 1410, Ap
c 4	24	1.2	341	12	US-10-033-528-1410	Sequence 1410, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 22:25:37 ; Search time 2958 Seconds
(without alignments)
11415.683 Million cell updates/sec

Title: US-09-846-589A-9
Perfect score: 2085
Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
	1	2085	100.0	2120	11	AY104190	AY104190 Zea mays
c	2	566	27.1	577	10	AW000193	AW000193 614058H08
	3	521	25.0	624	10	AW065367	AW065367 614048G06
	4	505	24.2	581	10	AW065368	AW065368 614048G07
	5	452	21.7	636	10	AW065483	AW065483 614058H08
c	6	419	20.1	470	9	AI947463	AI947463 614048G07
	7	387	18.6	586	10	AW563004	AW563004 660070H04
	8	368	17.6	451	13	BM498280	BM498280 952021B05
	9	365	17.5	548	13	BM498016	BM498016 952021B05
	10	337	16.2	522	13	BM428660	BM428660 952021B05
c	11	337	16.2	548	14	BQ667878	BQ667878 946101G05
	12	328	15.7	478	14	BQ667879	BQ667879 946101G05
c	13	290	13.9	594	10	AW600543	AW600543 660070H04
c	14	272	13.0	604	9	AI746204	AI746204 605082F05
	15	236	11.3	588	10	AW497943	AW497943 660042A12
c	16	233	11.2	504	10	AW498128	AW498128 660042A12
c	17	174	8.3	327	9	AI939893	AI939893 618026C01
	18	160	7.7	393	14	BQ778947	BQ778947 946115G02
c	19	144	6.9	207	17	BH412384	BH412384 1007026G1
	20	113	5.4	412	14	BQ282680	BQ282680 WHE3080_D
	21	113	5.4	547	10	BE593605	BE593605 WS1_98_F1
	22	104	5.0	508	9	AI649625	AI649625 486068G03
c	23	99	4.7	484	17	BH635759	BH635759 1008006G1
	24	96	4.6	584	14	BQ294221	BQ294221 1091026H1
	25	92	4.4	535	12	BG411263	BG411263 EM1_27_F0
c	26	65	3.1	615	9	AI622640	AI622640 486105A09
	27	54	2.6	359	14	BQ282168	BQ282168 WHE3055_F
	28	54	2.6	478	10	AW286571	AW286571 LG1_334_E
	29	54	2.6	533	10	AW286552	AW286552 LG1_334_C
	30	54	2.6	566	10	AW679266	AW679266 WS1_23_H0
	31	54	2.6	647	10	BE593197	BE593197 WS1_98_F1
	32	52	2.5	253	12	BG411643	BG411643 EM1_59_H0
c	33	43	2.1	338	9	AI600795	AI600795 486068G03
	34	41	2.0	244	10	AW679193	AW679193 WS1_23_H0
	35	37	1.8	590	12	BG410925	BG410925 EM1_27_F0
	36	35	1.7	609	10	AV833385	AV833385 AV833385
	37	35	1.7	614	13	BM135900	BM135900 WHE2619_H
	38	35	1.7	643	13	BJ463548	BJ463548 BJ463548
c	39	32	1.5	475	17	AZ858962	AZ858962 2M0164C22
	40	32	1.5	500	14	BQ839424	BQ839424 WHE4165_H
	41	32	1.5	502	10	BE497913	BE497913 WHE0958_G
	42	32	1.5	589	13	BJ245810	BJ245810 BJ245810
	43	32	1.5	598	10	BE499567	BE499567 WHE0962_H
	44	32	1.5	653	14	BQ838563	BQ838563 WHE2912_A
	45	30	1.4	600	17	AZ859302	AZ859302 2M0164C22

No hits long enough
to be prior art

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 18:25:41 ; Search time 5450 Seconds
(without alignments)
11133.826 Million cell updates/sec

Title: US-09-846-589A-9
Perfect score: 2085
Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

Seg Search Summary
for Seg ID No: 9

Identity

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID	Description
	No.	Score	Match	Length				
	1	2085	100.0	2085	6	AR160636	AR160636	Sequence
	2	1141.4	54.7	1957	6	AR160637	AR160637	Sequence
	3	456.2	21.9	2183	6	AR160638	AR160638	Sequence
	4	442.6	21.2	1867	8	AF370143	AF370143	Arabidops
	5	439.8	21.1	1513	8	AY051059	AY051059	Arabidops
	6	353	16.9	142373	2	AC122149	AC122149	Oryza sat
	7	305.8	14.7	11615	1	AE010214	AE010214	Pyrococcu
c	8	296.6	14.2	233000	1	AP000003	AP000003	Pyrococcu
c	9	277.6	13.3	323930	1	AP003194	AP003194	Clostridi
c	10	276.6	13.3	9552	1	AE013173	AE013173	Thermoana
	11	275.6	13.2	304290	1	CNSPAX05	AJ248287	Pyrococcu
	12	275.6	13.2	349980	6	AX041921	AX041921	Sequence
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	14	268.8	12.9	1922	1	BSCTS	X73989	B.subtilis
	15	268.8	12.9	6357	1	BACGLUSYN	L14580	Bacillus su
	16	268.8	12.9	180136	1	BAC180K	D26185	B. subtilis
	17	268.8	12.9	213080	1	BSUB0001	Z99104	Bacillus su
	18	267.2	12.8	92407	6	AX067461	AX067461	Sequence
	19	262.2	12.6	12851	1	AE013714	AE013714	Yersinia
c	20	262.2	12.6	205050	1	AJ414155	AJ414155	Yersinia
c	21	258	12.4	11515	1	AE004260	AE004260	Vibrio ch
	22	255.2	12.2	15086	1	CST130879	AJ130879	Clostridi
c	23	254.6	12.2	10461	1	U32693	U32693	Haemophilus
	24	253.2	12.1	1416	6	AX413912	AX413912	Sequence
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	29	251.6	12.1	1401	6	AR016529	AR016529	Sequence
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	31	251.6	12.1	301050	1	AP003130	AP003130	Staphyloc
	32	251.6	12.1	325350	1	AP004823	AP004823	Staphyloc
	33	251.6	12.1	343590	1	AP003359	AP003359	Staphyloc

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	36	251	12.0	19985	1	AE008721	AE008721 Salmonell
c	37	250.2	12.0	11541	1	AE007813	AE007813 Clostridi
	38	250.2	12.0	300150	1	AP001507	AP001507 Bacillus
	39	247.4	11.9	2633	6	AX416651	AX416651 Sequence
c	40	244.4	11.7	293181	1	AP001119	AP001119 Buchnera
	41	243.6	11.7	224650	1	AL596164	AL596164 Listeria
	42	243.6	11.7	349980	6	AX415067	AX415067 Sequence
	43	242	11.6	1399	6	AX432748	AX432748 Sequence
c	44	241.6	11.6	348350	1	AP003584	AP003584 Nostoc sp
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ALIGNMENTS

RESULT 1

AR160636

LOCUS AR160636 2085 bp DNA linear PAT 17-OCT-2001

DEFINITION Sequence 9 from patent US 6255090.

ACCESSION AR160636

VERSION AR160636.1 GI:16224963

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2085)

AUTHORS Famodu,L.O., Orozco,E.M. Jr. and Rafalski,J.Antoni.

TITLE Plant aminoacyl-tRNA synthetase

JOURNAL Patent: US 6255090-A 9 03-JUL-2001;

FEATURES Location/Qualifiers

source 1..2085

/organism="unknown"

BASE COUNT 603 a 466 c 501 g 515 t

ORIGIN

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 17:24:05 ; Search time 437 Seconds
(without alignments)
10744.660 Million cell updates/sec

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Perfect score: 2085
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Scoring table: IDENTITY_NUC
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

From USPN 6255090

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3	456.2	21.9	2183	22	AAD07975	Soybean cysteinyl-
4	286.6	13.7	294	24	ABL72570	Corn tassel-derive
5	275.6	13.2	349980	22	AAH41226	Pyrococcus abyssi
6	267.2	12.8	92407	22	AAF28549	Genomic fragment #
7	253.2	12.1	1416	24	ABQ68090	Listeria monocytog
8	253.2	12.1	2944528	24	ABA03041	Listeria monocytog
9	251.6	12.1	1401	18	AAT72875	DNA encoding cyste
10	251.6	12.1	1401	19	AAV31108	Staphylococcus aur
11	251.6	12.1	1401	21	AAA39270	Staphylococcus aur
12	251.4	12.1	1440	24	ABN91828	Staphylococcus epi
c 13	251.4	12.1	3242	22	AAH54369	S. epidermidis gen
14	247.4	11.9	2633	24	ABQ70829	Listeria monocytog
c 15	244.4	11.7	640681	24	ABA92787	Buchnera sp. genom
16	243.8	11.7	1399	23	AAS52150	Staphylococcus aur
17	243.6	11.7	3011208	24	ABQ69245	Listeria innocua D
18	242	11.6	1399	24	ABK73872	Bacillus lichenifo
19	241.4	11.6	1142	21	AAC41815	Arabidopsis thalia
20	231.6	11.1	1341	24	ABN66316	Streptococcus poly
21	231.6	11.1	2155561	24	ABN71527	Streptococcus poly
22	231	11.1	1163020	24	ABQ67197	Listeria innocua c
c 23	227.6	10.9	6876	18	AAV74497	Staphylococcus aur
c 24	223.4	10.7	2365589	24	ABA90521	Genomic sequence o
25	218.2	10.5	1344	18	AAT97093	Streptococcus pneu
c 26	218.2	10.5	28882	19	AAV52273	Streptococcus pneu
c 27	213.4	10.2	10636	20	AAH13011	Enterococcus faeca
28	198.6	9.5	1605	24	ABQ69120	Listeria monocytog
29	194.6	9.3	1341	24	ABN66317	Streptococcus poly
c 30	186.4	8.9	92934	21	AAA81473	N. meningitidis pa
c 31	186.4	8.9	172325	21	AAF21613	Neisseria meningit
c 32	186.4	8.9	837096	21	AAA81489	N. meningitidis pa
c 33	176.8	8.5	4403765	22	AAI99683	Mycobacterium tube
34	170.6	8.2	1380	22	AAH67868	C glutamicum codin
c 35	170.6	8.2	349980	22	AAH68533	C glutamicum codin
36	139.6	6.7	749	24	ABK78323	Bacillus clausii g
37	134.2	6.4	4353	23	AAS75024	DNA encoding novel
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39	133.6	6.4	3380	22	AAH54470	S. epidermidis gen
c 40	129.6	6.2	13336	23	AAS59554	Propionibacterium
41	116.4	5.6	1398	18	AAV25143	H. pylori cytoplas
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ALIGNMENTS

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 17:27:25 ; Search time 82 Seconds
(without alignments)
7797.818 Million cell updates/sec

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Perfect score: 2085
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Scoring table: IDENTITY_NUC
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Listing first 45 summaries

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SUMMARIES

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c	16	106	5.1	1360	4	US-08-858-207A-65	Sequence 65, Appl
	17	89.8	4.3	2083	4	US-09-221-017B-938	Sequence 938, App
c	18	71.8	3.4	7218	1	US-08-232-463-14	Sequence 14, Appl
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	41	60.4	2.9	234	1	US-08-469-802B-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1

US-09-352-990-9

; Sequence 9, Application US/09352990

; Patent No. 6255090

; GENERAL INFORMATION:

; APPLICANT: Famodu, Layo O.

; APPLICANT: Orozco, Buddy

; APPLICANT: Rafalski, Antoni

; TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase

; FILE REFERENCE: BB-1191

; CURRENT APPLICATION NUMBER: US/09/352,990

; CURRENT FILING DATE: 1999-07-14

; EARLIER APPLICATION NUMBER: 60/092,866

; EARLIER FILING DATE: July 15, 1998

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 9

; LENGTH: 2085

; TYPE: DNA

GenCore version 5.1.3
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	16	62.8	3.0	553	10	US-09-920-300A-1461	Sequence 1461, Ap
	17	62.8	3.0	553	12	US-10-033-528-1461	Sequence 1461, Ap
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c	26	56.8	2.7	8895	10	US-09-764-853-887	Sequence 887, App
c	27	56.8	2.7	8895	10	US-09-764-853-937	Sequence 937, App
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	36	54.2	2.6	6878	10	US-09-735-367B-1	Sequence 1, Appli
c	37	54	2.6	521	10	US-09-815-343-422	Sequence 422, App
c	38	53.8	2.6	272	10	US-09-864-761-18684	Sequence 18684, A
	39	53.6	2.6	270	9	US-10-007-557-8	Sequence 8, Appli
	40	52.4	2.5	366	10	US-09-960-352-2926	Sequence 2926, Ap
c	41	52.4	2.5	512	10	US-09-864-761-25347	Sequence 25347, A
c	42	52.4	2.5	575	10	US-09-864-761-8628	Sequence 8628, Ap
	43	52.4	2.5	1143	9	US-09-938-842A-1399	Sequence 1399, Ap
	44	51.6	2.5	2031	10	US-09-801-368-301	Sequence 301, App
	45	50.6	2.4	7326	12	US-10-109-886-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-294-093B-1944

; Sequence 1944, Application US/09294093B

; Patent No. US20010051335A1

; GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath, V.

; APPLICANT: Ito, Laura, Y.

; APPLICANT: Sherman, Bradley, K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

; FILE REFERENCE: PL-0009 US

cited to PTO-892

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2003, 19:16:51 ; Search time 2957 Seconds
(without alignments)
11419.543 Million cell updates/sec

Title: US-09-846-589A-9
Perfect score: 2085
Sequence: 1 ggaaaccgtgtttcgacggg.....tatacttgacagttgactcc 2085

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description
	1	2085	100.0	2120	11	AY104190 Zea mays
	2	603.6	28.9	624	10	AW065367 614048G06
	3	582.6	27.9	636	10	AW065483 614058H08
c	4	568.4	27.3	577	10	AW000193 614058H08
	5	563	27.0	581	10	AW065368 614048G07
	6	554.4	26.6	586	10	AW563004 660070H04
	7	546.6	26.2	588	10	AW497943 660042A12
c	8	534.6	25.6	548	14	BQ667878 946101G05
	9	530.8	25.5	548	13	BM498016 952021B05
	10	506.4	24.3	522	13	BM428660 952021B05
c	11	505.6	24.2	594	10	AW600543 660070H04
	12	494.8	23.7	647	10	BE593197 WS1_98_F1
c	13	489.4	23.5	604	9	AI746204 605082F05
c	14	468.4	22.5	470	9	AI947463 614048G07
	15	460.6	22.1	643	13	BJ463548 BJ463548
	16	457.4	21.9	535	12	BG411263 EM1_27_F0
	17	456.4	21.9	652	14	BQ465217 HU02P15r
c	18	448	21.5	504	10	AW498128 660042A12
	19	444.4	21.3	547	10	BE593605 WS1_98_F1
	20	444.4	21.3	609	10	AV833385 AV833385
	21	437.4	21.0	451	13	BM498280 952021B05
	22	428	20.5	614	13	BM135900 WHE2619_H
	23	416.2	20.0	478	14	BQ667879 946101G05
	24	388.2	18.6	589	13	BJ245810 BJ245810
	25	384.2	18.4	533	10	AW286552 LG1_334_C
	26	375.6	18.0	595	14	BQ468212 HP01G15T
	27	361.6	17.3	393	14	BQ778947 946115G02
	28	360.4	17.3	693	9	AL507468 AL507468
c	29	345	16.5	615	9	AI622640 486105A09
	30	344.8	16.5	500	14	BQ839424 WHE4165_H
	31	333.6	16.0	412	14	BQ282680 WHE3080_D
	32	332.4	15.9	478	10	AW286571 LG1_334_E
c	33	322.2	15.5	327	9	AI939893 618026C01
c	34	321.6	15.4	692	13	BJ466496 BJ466496
	35	306.2	14.7	653	14	BQ838563 WHE2912_A
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	38	302.4	14.5	566	10	AW679266 WS1_23_H0
	39	302.4	14.5	700	9	AL507494 AL507494
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c	41	296.8	14.2	606	14	BQ169075 WHE2158_A
	42	293	14.1	611	12	BG451468 NF110F10D
	43	292.6	14.0	600	12	BG521662 13-20 Ste
	44	289.8	13.9	480	9	AJ466919 AJ466919
	45	283.4	13.6	629	14	BQ490648 96-E01178

ALIGNMENTS